1644

RECEIVED

SEP 2 6 2002

TECH CENTER 1600/2900

P#13   1600

P.6

```
RAW SEQUENCE LISTING                    DATE: 09/19/2002
PATENT APPLICATION:  US/09/476,485A     TIME: 16:25:24

         Input Set : A:\108236-119.ST25.txt
         Output Set: N:\CRF4\09192002\I476485A.raw
```

ENTERED

```
 4 <110> APPLICANT: Colucci, M. Gabriella
 5        Chrispeels, Maarten J.
 6        Moore, Jeffrey G.
 8 <120> TITLE OF INVENTION: Progenitor Cell Preservation Factors and Methods for
 9        and Products of Their Use
11 <130> FILE REFERENCE: 108236.119
13 <140> CURRENT APPLICATION NUMBER: US 09/476,485A
14 <141> CURRENT FILING DATE: 2000-12-22
16 <150> PRIOR APPLICATION NUMBER: US 08/881,189
17 <151> PRIOR FILING DATE: 1997-06-24
19 <160> NUMBER OF SEQ ID NOS: 57
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 939
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: D1-FRIL.
32 <400> SEQUENCE: 1
33 gcacagtcat tgtcatttag tttcaccaag tttgatccta accaagagga tcttatcttc      60
35 caaggtcatg ccacttctac aaacaatgtc ttacaagtca ccaagttaga cagtgcagga     120
37 aaccctgtga gttctagtgc gggaagagtg ttatattctg caccattgcg cctttgggaa     180
39 gactctgcgg tattgacaag ctttgacacc attatcaact ttgaaatctc aacaccttac     240
41 acttctcgta tagctgatgg cttggccttc ttcattgcac cacctgactc tgtcatcagt     300
43 tatcatggtg gttttcttgg actctttccc aacgcaaaca ctctcaacaa ctcttccacc     360
45 tctgaaaacc aaaccaccac taaggctgca tcaagcaacg ttgttgctgt tgaatttgac     420
47 acctatctta atcccgatta tggtgatcca aactacatac acatcggaat tgacgtcaac     480
49 tctattagat ccaaggtaac tgctaagtgg gactggcaaa atgggaaaat agccactgca     540
51 cacattagct ataactctgt ctctaaaaga ctatctgtta ctagttatta tgctgggagt     600
53 aaacctgcga ctctctccta tgatattgag ttacatacag tgcttcctga atgggtcaga     660
55 gtagggttat ctgcttcaac tggacaagat aaagaaagaa ataccgttca ctcatggtct     720
57 ttcacttcaa gcttgtggac caatgtggcg aagaaggaga atgaaaacaa gtatattaca     780
59 agaggcgttc tgtgatgata tatgtgtatc aatgattttc tatgttataa gcatgtaatg     840
61 tgcgatgagt caataatcac aagtacagtg tagtacttgt atgttgtttg tgtaagagtc     900
63 agtttgcttt taataataac aagtgcagtt agtacttgt                            939
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 264
69 <212> TYPE: PRT
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: D1-FRIL.
76 <400> SEQUENCE: 2
78 Ala Gly Ser Leu Ser Phe Ser Phe Thr Lys Phe Asp Pro Asn Gln Glu
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/476,485A

DATE: 09/19/2002
TIME: 16:25:24

Input Set : A:\108236-119.ST25.txt
Output Set: N:\CRF4\09192002\I476485A.raw

```
 79 1               5               10              15
 81 Asp Leu Ile Phe Gln Gly His Ala Thr Ser Thr Asn Asn Val Leu Gln
 82          20              25              30
 84 Val Thr Lys Leu Asp Ser Ala Gly Asn Pro Val Ser Ser Ser Ala Gly
 85          35              40              45
 87 Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu Trp Glu Asp Ser Ala Val
 88      50              55              60
 90 Leu Thr Ser Phe Asp Thr Ile Ile Asn Phe Glu Ile Ser Thr Pro Tyr
 91 65              70              75              80
 93 Thr Ser Arg Ile Ala Asp Gly Leu Ala Phe Phe Ile Ala Pro Pro Asp
 94              85              90              95
 96 Ser Val Ile Ser Tyr His Gly Gly Phe Leu Gly Leu Phe Pro Asn Ala
 97              100             105             110
 99 Asn Thr Leu Asn Asn Ser Ser Thr Ser Glu Asn Gln Thr Thr Thr Lys
100          115             120             125
102 Ala Ala Ser Ser Asn Val Val Ala Val Glu Phe Asp Thr Tyr Leu Asn
103          130             135             140
105 Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile Gly Ile Asp Val Asn
106 145             150             155             160
108 Ser Ile Arg Ser Lys Val Thr Ala Lys Trp Asp Trp Gln Asn Gly Lys
109              165             170             175
111 Ile Ala Thr Ala His Ile Ser Tyr Asn Ser Val Ser Lys Arg Leu Ser
112          180             185             190
114 Val Thr Ser Tyr Tyr Ala Gly Ser Lys Pro Ala Thr Leu Ser Tyr Asp
115          195             200             205
117 Ile Glu Leu His Thr Val Leu Pro Glu Trp Val Arg Val Gly Leu Ser
118      210             215             220
120 Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn Thr Val His Ser Trp Ser
121 225             230             235             240
123 Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Lys Glu Asn Glu Asn
124          245             250             255
126 Lys Tyr Ile Thr Arg Gly Val Leu
127          260
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 1005
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Nucleic acid sequence of the naturally-occurring D1-FRIL
protein.
139 <400> SEQUENCE: 3
140 atggcttcct ccaacttact caccctagcc ctcttccttg tgcttctcac ccacgcaaac      60
142 tcagccgcac agtcattgtc atttagtttc accaagtttg atcctaacca agaggatctt     120
144 atcttccaag gtcatgccac ttctacaaac aatgtcttac aagtcaccaa gttagacagt     180
146 gcaggaaacc ctgtgagttc tagtgcggga agagtgttat attctgcacc attcgccctt     240
148 tgggaagact ctgcggtatt gacaagcttt gacaccatta tcaactttga aatctcaaca     300
150 ccttacactt ctcgtatagc tgatggcttg gccttcttca ttgcaccacc tgactctgtc     360
152 atcagttatc atggtggttt tcttggactc tttcccaacg caaacactct caacaactct     420
154 tccacctctg aaaaccaaac caccactaag gctgcatcaa gcaacgttgt tgctgttgaa     480
156 tttgacacct atcttaatcc cgattatggt gatccaaact acatacacat cggaattgac     540
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/476,485A

DATE: 09/19/2002
TIME: 16:25:24

Input Set : A:\108236-119.ST25.txt
Output Set: N:\CRF4\09192002\I476485A.raw

```
158 gtcaactcta ttagatccaa ggtaactgct aagtgggact ggcaaaatgg gaaaatagcc    600
160 actgcacaca ttagctataa ctctgtctct aaaagactat ctgttactag ttattatgct    660
162 gggagtaaac ctgcgactct ctcctatgat attgagttac atacagtgct tcctgaatgg    720
164 gtcagagtag ggttatctgc ttcaactgga caagataaag aaagaaatac cgttcactca    780
166 tggtctttca cttcaagctt gtggaccaat gtggcgaaga aggagaatga aaacaagtat    840
168 attacaagag gcgttctgtg atgatatatg tgtatcaatg attttctatg ttataagcat    900
170 gtaatgtgcg atgagtcaat aatcacaagt acagtgtagt acttgtatgt tgtttgtgta    960
172 agagtcagtt tgcttttaat aataacaagt gcagttagta cttgt               1005
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 22
177 <212> TYPE: PRT
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Signal sequence from the FRIL family isolated from
182         Dolichos lab lab
185 <400> SEQUENCE: 4
187 Met Ala Ser Ser Asn Leu Leu Thr Leu Ala Leu Phe Leu Val Leu Leu
188 1               5                   10                  15
190 Thr His Ala Asn Ser Ala
191             20
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 914
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Pv-FRIL.
203 <400> SEQUENCE: 5
204 gctcagtcat tatcttttaa ctttaccaag tttgatcttg accaaaaaga tcttatcttc     60
206 caaggtgatg ccacttctac aaacaatgtc ttacaactca ctaagttaga cagtggagga    120
208 aaccctgtgg gtgctagtgt gggaagagtg ttattctctg caccatttca tctttgggaa    180
210 aactctatgg cagtgtcaag ctttgaaact aatctcacca ttcaaatctc aacacctcac    240
212 ccttattatg cagctgatgg ctttgccttc ttccttgcac cacatgacac tgtcatccct    300
214 ccaaattctt ggggcaaatt ccttggactc tactcaaacg ttttcagaaa ctcccccacc    360
216 tctgaaaacc aaagctttgg tgatgtcaat actgactcaa gagttgttgc tgtcgaattt    420
218 gacaccttcc ctaatgccaa tattgatcca aattacagac acattggaat cgatgtgaac    480
220 tctattaagt ccaaggaaac tgctaggtgg gagtggcaaa atgggaaaac ggccactgca    540
222 cgcatcagct ataactctgc ctctaaaaaa tcaactgtta ctacgtttta tcctgggatg    600
224 gaagttgtgg ctctctccca tgatgttgac ttacatgcag agcttcctga atgggttaga    660
226 gtagggttat ctgcttcaac tggagaggag aaacaaaaaa ataccattat ctcatggtct    720
228 ttcacttcaa gcttgaagaa caacgaggtg aaggagccga agaagacat gtatattgca    780
230 aacgttgtgc gatcatatac atggatcaat gacgttctat cttatataag caataaataa    840
232 atgtatgatg cactcaataa taatcacaag tacgtacggt gtagtacttg tatgttgttt    900
234 atgaaaaaaa aaaa                                                     914
238 <210> SEQ ID NO: 6
239 <211> LENGTH: 303
240 <212> TYPE: PRT
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Pv-FRIL.
```

RAW SEQUENCE LISTING   DATE: 09/19/2002
PATENT APPLICATION: US/09/476,485A   TIME: 16:25:24

Input Set : A:\108236-119.ST25.txt
Output Set: N:\CRF4\09192002\I476485A.raw

247 <400> SEQUENCE: 6
249 Ala Gln Ser Leu Ser Phe Asn Phe Thr Lys Phe Asp Leu Asp Gln Lys
250 1   5   10   15
252 Asp Leu Ile Phe Gln Gly Asp Ala Thr Ser Thr Asn Asn Val Leu Gln
253   20   25   30
255 Leu Thr Lys Leu Asp Ser Gly Gly Asn Pro Val Gly Ala Ser Val Gly
256   35   40   45
258 Arg Val Leu Phe Ser Ala Pro Phe His Leu Trp Glu Asn Ser Met Ala
259   50   55   60
261 Val Ser Ser Phe Glu Thr Asn Leu Thr Ile Gln Ile Ser Thr Pro His
262 65   70   75   80
264 Pro Tyr Tyr Ala Ala Asp Gly Phe Ala Phe Phe Leu Ala Pro His Asp
265   85   90   95
267 Thr Val Ile Pro Pro Asn Ser Trp Gly Lys Phe Leu Gly Leu Tyr Ser
268   100   105   110
270 Asn Val Phe Arg Asn Ser Pro Thr Ser Glu Asn Gln Ser Phe Gly Asp
271   115   120   125
273 Val Asn Thr Asp Ser Arg Val Val Ala Val Glu Phe Asp Thr Phe Pro
274   130   135   140
276 Asn Ala Asn Ile Asp Pro Asn Tyr Arg His Ile Gly Ile Asp Val Asn
277 145   150   155   160
279 Ser Ile Lys Ser Lys Glu Thr Ala Arg Trp Glu Trp Gln Asn Gly Lys
280   165   170   175
282 Thr Ala Thr Ala Arg Ile Ser Tyr Asn Ser Ala Ser Lys Lys Ser Thr
283   180   185   190
285 Val Thr Thr Phe Tyr Pro Gly Met Glu Val Val Ala Leu Ser His Asp
286   195   200   205
288 Val Asp Leu His Ala Glu Leu Pro Glu Trp Val Arg Val Gly Leu Ser
289   210   215   220
291 Ala Ser Thr Gly Glu Glu Lys Gln Lys Asn Thr Ile Ile Ser Trp Ser
292 225   230   235   240
294 Phe Thr Ser Ser Leu Lys Asn Asn Glu Val Lys Glu Pro Lys Glu Asp
295   245   250   255
297 Met Tyr Ile Ala Asn Val Val Arg Ser Tyr Thr Trp Ile Asn Asp Val
298   260   265   270
300 Leu Ser Tyr Ile Ser Asn Lys Met Tyr Asp Ala Leu Asn Asn Asn His
301   275   280   285
303 Lys Tyr Val Arg Cys Ser Thr Cys Met Leu Phe Met Lys Lys Lys
304   290   295   300
307 <210> SEQ ID NO: 7
308 <211> LENGTH: 678
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: YamFril partial mRNA sequence.
316 <400> SEQUENCE: 7
317 acgaagttcg acagcgacca aaaggatctt atgttccaag gtcataccat ttctagcagc   60
319 aatgtcatac aactcaccaa gttagacagt aatggaaacc ctgtgagtac cagtgtggga   120
321 agagtgttat actctgcacc attgcgcctt tgggaaagct ctacagtagt gtcaaccttt   180

```
323 gagaccactt tcacctttca aatctcaaca ccttacacta gtcctcctgg tgatgggctc   240
325 gccttcttcc ttgcaccata tgacactgtc atccctccaa attctgctgg caatcttctt   300
327 ggactctttc ctaacttaaa tgctttaaga aactccacca ccagtaaaga aaccactatt   360
329 gatgtcaatg ctgcatctaa caacgttgtt gccgttgaat ttgacaccta ccctaacgac   420
331 aatattggtg atccaagata caaacacatt ggaatcgatg tcaactctat caggtccaag   480
333 gcaactgttg cgtgggactg gcaaaatggg aaaacagcca ctgcacacat cagctataac   540
335 tctgcctcta aaagactatc tgttactact ttttatcctg ggggtaaagc tgtgagtctt   600
337 tcccatgacg ttgagctcac tcaagtgctt cctcaatgga ttagagtagg gttctctgct   660
339 tcaacaggat tagagaaa                                                  678
```

343 <210> SEQ ID NO: 8
344 <211> LENGTH: 234
345 <212> TYPE: PRT
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: YamFril deduced amino acid squence.
352 <400> SEQUENCE: 8

```
354 Ala Gln Ser Val Ser Phe Thr Phe Thr Lys Phe Asp Ser Asp Gln Lys
355 1               5                   10                  15
357 Asp Leu Met Phe Gln Gly His Thr Ile Ser Ser Ser Asn Val Ile Gln
358             20                  25                  30
360 Leu Thr Lys Leu Asp Ser Asn Gly Asn Pro Val Ser Thr Ser Val Gly
361         35                  40                  45
363 Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu Trp Glu Ser Ser Thr Val
364     50                  55                  60
366 Val Ser Thr Phe Glu Thr Thr Phe Thr Phe Gln Ile Ser Thr Pro Tyr
367 65                  70                  75                  80
369 Thr Ser Pro Pro Gly Asp Gly Leu Ala Phe Phe Leu Ala Pro Tyr Asp
370             85                  90                  95
372 Thr Val Ile Pro Pro Asn Ser Ala Gly Asn Leu Leu Gly Leu Phe Pro
373             100                 105                 110
375 Asn Leu Asn Ala Leu Arg Asn Ser Thr Thr Ser Lys Glu Thr Thr Ile
376         115                 120                 125
378 Asp Val Asn Ala Ala Ser Asn Asn Val Val Ala Val Glu Phe Asp Thr
379     130                 135                 140
381 Tyr Pro Asn Asp Asn Ile Gly Asp Pro Tyr Arg Lys His Ile Gly Ile
382 145                 150                 155                 160
384 Asp Val Asn Ser Ile Arg Ser Lys Ala Thr Val Ala Trp Asp Trp Gln
385             165                 170                 175
387 Asn Gly Lys Thr Ala Thr Ala His Ile Ser Tyr Asn Ser Ala Ser Lys
388         180                 185                 190
390 Arg Leu Ser Val Thr Thr Phe Tyr Pro Gly Gly Lys Ala Val Ser Leu
391         195                 200                 205
393 Ser His Asp Val Glu Leu Thr Gln Val Leu Pro Gln Trp Ile Arg Val
394     210                 215                 220
396 Gly Phe Ser Ala Ser Thr Gly Leu Glu Lys
397 225                 230
```

400 <210> SEQ ID NO: 9
401 <211> LENGTH: 15
402 <212> TYPE: PRT

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/19/2002
PATENT APPLICATION: US/09/476,485A   TIME: 16:25:25

Input Set : A:\108236-119.ST25.txt
Output Set: N:\CRF4\09192002\I476485A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:10; Xaa Pos. 14
Seq#:11; N Pos. 3,6,9,12,15,18,21
Seq#:12; N Pos. 3,6,9,15
Seq#:16; N Pos. 3,6,9,12,15
Seq#:24; Xaa Pos. 7
Seq#:31; Xaa Pos. 7
Seq#:32; Xaa Pos. 7
Seq#:33; Xaa Pos. 12
Seq#:34; Xaa Pos. 7
Seq#:36; N Pos. 18
```

VERIFICATION SUMMARY   DATE: 09/19/2002
PATENT APPLICATION: US/09/476,485A   TIME: 16:25:25

Input Set : A:\108236-119.ST25.txt
Output Set: N:\CRF4\09192002\I476485A.raw

```
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:925 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1121 M:283 W: Missing Blank Line separator, <220> field identifier
```